Author index

Abbo, S. *see* Liu, B.
Adam, G., Mullen, J.A. and Kindle, K.L. *Retrofitting YACs for direct DNA transfer into plant cells* 1349
Afonso, C.L. *see* Grebenok, R.J.
Ahmad, M. and Cashmore, A.R. *The blue-light receptor cryptochrome 1 shows functional dependence on phyrochrome A or phytochrome B in* Arabidopsis thaliana 421
Ait-Ali, T., Swain, S.M., Reid, J.B., Sun, T.-P. and Kamiya, Y. *The LS locus of pea encodes the gibberellin biosynthesis enzyme* ent-*kaurene synthase A* 443
Akaike, M. *see* Mita, S.
Albersheim, P. *see* Ham, K.-S.
Albert, S., Delseny, M. and Devic, M. BANYULS, *a novel negative regulator of flavonoid biosynthesis in the* Arabidopsis *seed coat* 289
Allen, P.V. *see* Moehs, C.P.
Altabella, T. *see* Masgrau, C.
Aoyama, T. and Chua, N.-H. *A glucocorticoid-meditated transcriptional induction system in transgenic plants* 605
Armstrong, G.A. *see* Burkhardt, P.K.
Assmann, S.M. *see* Maathuis, F.J.M.
Aubert, S., Bigny, R., Day, D.A., Whelan, J. and Douce, R. *Induction of alternative oxidase synthesis by herbicides inhibiting branched-chain amino acid synthesis* 649

Bachmair, A. *see* Wanzenbock, E.-M.
Bak, S., Kahn, R.A., Olsen, C.E. and Halkier, B.A. *Cloning and expression in* Escherichia coli *of the obtusifoliol 14α-demethylase of* Sorghum bicolor *(L.) Moench, a cytochrome P450 orthologous to the sterol 14α-demethylases (CYP51) from fungi and mammals* 191
Baker, B. *see* Wirtz, U.
Balsamo, R.A. *see* Wang, T.-W.
Barroso, C. *see* Gotor, C.
Bassuner, B. *see* Kononov, M.E.
Bauer, P. *see* Coba de la Pena, T.
Beck, C.F. *see* Haring, M.A.
Beecher, B. *see* Zurek, D.M.
Belknap, W.R. *see* Moehs, C.P.
Belzile, F. *see* Jarvis, P.
Belzile, F. *see* Jarvis, P.
Bertekap, R.L. *see* Terzaghi, W.B.
Besford, R.T. *see* Masgrau, C.
Bethke, P.C. and Jones, R.L. *Reversible protein phosphorylation regulates the activity of the slow-vacuolar ion channel* 1227
Betzner, A.S., Oakes, M.P. and Huttner, E. *Transfer RNA-mediated suppression of amber stop codons in transgenic* Arabidopsis thaliana 587
Beveridge, C.A., Murfet, I.C., Kerhoas, L., Sotta, B., Miginiac, E. and Rameau, C. *The shoot controls zeatin riboside export from pea roots. Evidence from the branching mutant rms4* 339
Beyer, P. *see* Burkhardt, P.K.
Bigny, R. *see* Aubert, S.
Bogdanova, N. and Hell, R. *Cysteine synthesis in plants: protein–protein interactions of serine acetyltransferase from* Arabidopsis thaliana 251
Bogsch, E. *see* Mould, R.M.
Bogusz, D. *see* Franche, C.
Borg, S., Brandstrum, B., Jensen, T.J. and Poulsen, C. *Identification of new protein species among 33 different small GTP-binding proteins encoded by cDNAs from* Lotus japonicus, *and expression of corresponding mRNAs in developing root nodules* 237
Boudet, A.-M. *see* Lacombe, E.
Bowen, B.A. *see* Kosslak, R.M.
Bowling, S.E. *see* Peirson, B.N.
Brandstrum, B. *see* Borg, S.
Brendel, V. *see* Carle-Urioste, J.C.
Brettell, R. *see* Tingay, S.
Brown, S. *see* Coba de la Pena, T.
Brown, S.E. *see* Lapitan, N.L.V.
Budde, I. *see* Fischer, R.
Burkhardt, P.K., Beyer, P., Wunn, J., Kloti, A., Armstrong, G.A., Schledz, M., von Lintig, J. and Potrykus, I. *Transgenic rice (*Oryza sativa*) endosperm expressing daffodil (*Narcissus pseudonarcissus*) phytoene synthase accumulates phytoene, a key intermediate of provitamin A biosynthesis* 1071
Burks, M. *see* Rogers, S.W.
Busk, P.K., Jensen, A.B. and Pages, M. *Regulatory elements in vivo in the promoter of the abscisic acid responsive gene* rab17 *from maize* 1285

Caboche, M. *see* Crete, P.
Caboche, M. *see* Scheible, W.-R.
Callis, J. *see* Sun, C.-W.
Cameron-Mills, V. *see* Rouster, J.
Carle-Urioste, J.C., Brendel, V. and Walbot, V. *A combinatorial role for exon, intron and splice site sequences in splicing in maize* 1253
Carpenter, T.B. *see* Hatfield, P.M.
Carrington, J.C. *see* Grebenok, R.J.
Cashmore, A.R. *see* Ahmad, M.
Cashmore, A.R. *see* Terzaghi, W.B.
Cejudo, F.J. *see* Gotor, C.
Chamberlin, M.A. *see* Kosslak, R.M.
Chang, M. *see* Chen, X.
Chapman, J.V. *see* Clark, L.J.
Chatterjee, M. and Martin, C. *Tam3 produces a suppressible allele of the DAG locus of* Antirrhinum majus *similar to Mu-suppressible alleles of maize* 759
Chen, J. *see* Wang, S.-M.
Chen, X., Chang, M., Wang, B. and Wu, R. *Cloning of a Ca^{2+}-ATPase gene and the role of cytosolic Ca^{2+} in the gibberellin-dependent signaling pathway in aleurone cells* 363
Chen, Z. *see* Takahashi, H.
Choisne, N., Martin-Canadell, A. and Small, I. *Transactivation of a target gene using a suppressor tRNA in transgenic tobacco plants* 597
Chu, B. *see* Wang, S.-M.
Chua, N.-H. *see* Aoyama, T.
Chung, H.J. *see* Kim, S.Y.
Clark, L.J., Hamilton, J.G.C., Chapman, J.V., Rhodes, M.J.C. and Hallahan, D.L. *Analysis of monoterpenoids in glandular trichomes of the catmint* Nepeta racemosa 1387
Coba de la Pena, T., Frugier, F., McKhann, H.I., Bauer, P., Brown, S., Kondorosi, A. and Crespi, M. *A carbonic anhydrase gene is induced in the nodule primordium and its cell-specific expression is controlled by the presence of* Rhizobium *during development* 407
Collinge, D.B. *see* Thordal-Christensen, H.
Conner, J.A., Tantikanjana, T., Stein, J.C., Kandasamy, M.K., Nasrallah, J.B. and Nasrallah, M.E. *Transgene-induced*

silencing of S-locus genes and related genes in Brassica 809
Connolly, E.L. *see* Learned, R.M.
Conrath, U., Silva, H. and Klessig, D.F. *Protein dephosphorylation mediates salicylic acid-induced expression of PR-1 genes in tobacco* 747
Cooke, R. *see* Gallois, P.
Cooke, R., Raynal, M., Laudie, M. and Delseny, M. *Identification of members of gene families in* Arabidopsis thaliana *by contig construction from partial cDNA sequences: 106 genes encoding 50 cytoplasmic ribosomal proteins* 1127
Coupe, S.A. and Deikman, J. *Characterization of a DNA-binding protein that interacts with 5′ flanking regions of two fruit-ripening genes* 1207
Coupland, G. *see* Long, D.
Crespi, M. *see* Coba de la Pena, T.
Crete, P., Caboche, M. and Meyer, C. *Nitrite reductase expressoin is regulated at the post-transcriptional level by the nitrogen source in* Nicotiana plumbaginifolia *and* Arabidopsis thaliana 625

Dammann, C., Rojo, R. and Sanchez-Serrano, J.J. *Abscisic acid and jasmonic acid activate wound-inducible genes in potato through separate, organ-specific signal transduction pathways* 773
Darvill, A.G. *see* Ham, K.-S.
Day, D.A. *see* Aubert, S.
De Buck, S. *see* De Neve, M.
De Neve, M., De Buck, S., Jacobs, A., Van Montagu, M. and Depicker, A. *T-DNA integration patterns in co-transformed plant cells suggest that T-DNA repeats orignate from co-integration of separate T-DNAs* 15
Dean, C. *see* Jarvis, P.
Dean, C. *see* Jarvis, P.
Dean, C. *see* Schmidt, R.
Deikman, J. *see* Coupe, S.A.
Delhaize, E. *see* Smith, F.W.
Delseny, M. *see* Albert, S.
Delseny, M. *see* Cooke, R.
Dempsey, D.A., Pathirana, M.S., Wobbe, K.K. and Klessig, D.F. *Identification of an* Arabidopsis *locus required for resistance to turnip crinkle virus* 301
Denecke, J. *see* Vidal, S.
Denmat, L.-A. *see* Gomord, V.
Depicker, A. *see* De Neve, M.
Despres, B. *see* Gallois, P.
Devic, M. *see* Albert, S.
Dietz, K.-J. *see* Tikhonova, L.I.
Diouf, D. *see* Franche, C.
Dixon, R.A. *see* Faktor, O.
Dong, B. *see* Smith, F.W.
Douce, R. *see* Aubert, S.
Draper, J. *see* Martin, D.J.
Du, H. *see* Takahashi, H.
Duhoux, E. *see* Terzaghi, W.B.

Ealing, P.M. *see* Smith, F.W.
Egawa, H. *see* Takano, M.
Ehness, R. and Roitsch, T. *Co-ordinated induction of mRNAs for extracellular invertase and a glucose transporter in* Chenopodium rubrum *by cytokinins* 539
Eimert, K. *see* Wang, S.-M.
El-Turk, J. *see* Savoure, A.
Ellis, B.E. *see* Orvar, B.L.
Ellis, B.E. *see* Orvar, B.L.
Emes, M.J. *see* Naeem, M.
Esnault, R. *see* Savoure, A.

Faktor, O., Loake, G., Dixon, R.A. and Lamb, C.J. *The G-box and H-box in a 39 bp region of French bean chalcone synthase promoter constitute a tissue-specific regulatory element* 1105
Farras, R. *see* Masgrau, C.
Faye, L. *see* Gomord, V.
Fejes, E. *see* Haizel, T.
Feldbrugge, M., Sprenger, M., Hahlbrock, K. and Weisshaar, B. *PcMYB1, a novel plant protein containing a DNA-binding domain with one MYB repeat, interacts* in vivo *with a light-regulatory promoter unit* 1079
Feldman, M. *see* Liu, B.
Feuillet, C., Schachermayr, G. and Keller, B. *Molecular cloning of a new receptor-like kinase gene encoded at the Lr10 disease resistant locus of wheat* 45
Fieg, S. *see* Tingay, S.
Firek, S. *see* Martin, D.J.
Fischer, R., Budde, I. and Hain, R. *Stilbene synthase gene expression causes changes in flower colour and male sterility in tobacco* 489
Fitchette-Laine, A.-C. *see* Gomord, V.
Flores, D. *see* Masgrau, C.
Franche, C., Diouf, D., Le, Q.V. and Bogusz, D. *Genetic transformation of the actinorhizal tree* Allocasuarina verticillata *by* Agrobacterium tumefaciens 897
Franke-van Dijk, M.E.I. *see* Risseeuw, R.
Friedman, M. *see* Moehs, C.P.
Frommer, W.B. *see* Martin, T.
Frugier, F. *see* Coba de la Pena, T.
Fry, S.C. *Novel 'dot-blot' assays for glycosyltransferases and glycosylhydrolases: optimization for xyloglucan endotransglycosylase (XET) activity* 1141
Fujimoto, S. *see* Kobayashi, Y.
Fukuda, H. *see* Ito, M.
Fukui, K. *see* Nakamura, T.
Funaki, Y. *see* Kobayashi, Y.

Galbraith, D.W. *see* Grebenok, R.J.
Gallois, P., Makishima, T., Hecht, V., Despres, B., Laudie, M., Nishimoto, T. and Cooke, R. *An* Arabidopsis thaliana *cDNA complementing a hamster apoptosis suppressor mutant* 1325
Gelvin, S.B. *see* Kononov, M.E.
Gherbi, H. *see* Terzaghi, W.B.
Giraudat, J. *see* Parcy, F.
Gobe, C. *see* Terzaghi, W.B.
Goffner, D. *see* Lacombe, E.
Gomez, I. *see* Stange, C.
Gomord, V., Denmat, L.-A., Fitchette-Laine, A.-C., Satiat-Jeunemaitre, B., Hawes, C. and Faye, L. *The C-terminal HDEL sequence is sufficient for retention of secretory proteins in the endoplasmic reticulum (ER) but promotes vacuolar targeting of proteins that escape the ER* 313
Gong, F.C. *see* Grebenok, R.J.
Goodrich, J. *see* Long, D.
Gosink, M.M. *see* Hatfield, P.M.
Gotor, C., Cejudo, F.J., Barroso, C. and Vega, J.M. *Tissue-specific expression of ATCYS-3A, a gene encoding the cytosolic isoform of* O-acetylserine(thiol)lyase *in* Arabidopsis 347
Granell, A. *see* Orzaez, D.

Gray, J.C. *see* Mould, R.M.
Gray, J.C. *see* Webster, C.I.
Grebenok, R.J., Pierson, E., Lambert, G.M., Gong, F.C., Afonso, C.L., Haldeman-Cahill, R., Carrington, J.C. and Galbraith, D.W. *Green-fluorescent protein fusions for efficient characterization of nuclear targeting* 573
Grima-Pettenati, J. *see* Lacombe, E.

Hahlbrock, K. *see* Feldbrugge, M.
Hain, R. *see* Fischer, R.
Haizel, T., Merkle, T., Pay, A., Fejes, E. and Nagy, F. *Characterization of proteins that interact with the GTP-bound form of the regulatory GTPase Ran in* Arabidopsis 93
Haldeman-Cahill, R. *see* Grebenok, R.J.
Halkier, B.A. *see* Bak, S.
Hallahan, D.L. *see* Clark, L.J.
Ham, K.-S., Wu, S.-C., Darvill, A.G. and Albersheim, P. *Fungal pathogens secrete an inhibitor protein that distinguishes isoforms of plant pathogenesis-related endo-β-1,3-glucanases* 169
Hamilton, J.G.C. *see* Clark, L.J.
Hanson, M.R. *see* Kohler, R.H.
Haring, M.A. and Beck, C.F. *A promoter trap for* Chlamydomonas reinhardtii*: development of a gene cloning method using 5′ RACE-based probes* 1341
Harrington, S.E. *see* Meijer, A.H.
Hashimoto, J. *see* Ito, M.
Hata, S. *see* Ito, M.
Hatfield, P.M., Gosink, M.M., Carpenter, T.B. and Vierstra, R.D. *The ubiquitin-activating enzyme (E1) gene family in* Arabidopsis thaliana 213
Hawes, C. *see* Gomord, V.
Hawkins, S. *see* Lacombe, E.
Hecht, V. *see* Gallois, P.
Hell, R. *see* Bogdanova, N.
Hellmann, H. *see* Martin, T.
Herman, R. *see* Sarmiento, C.
Hoge, J.H.C. *see* Meijer, A.H.
Holuigue, L. *see* Stange, C.
Hooykaas, P.J.J. *see* Risseeuw, R.
Hooykaas, P.J.J. *see* Schlaman, H.R.M.
Huang, A.H.C. *see* Wang, T.-W.
Huang, B.-Q. *see* Sheridan, W.F.
Huttner, E. *see* Betzner, A.S.

Iba, K. *see* Inada, H.
Ikeda, J. *see* Takano, M.
Inada, H., Seki, M., Morikawa, H., Nishimura, M. and Iba, K. *Existence of three regulatory regions each containing a highly conserved motif in the promoter of plastid-encoded RNA polymerase gene (*rpoB*)* 883
Ingersoll, J. *see* Suzuki, H.
Irish, E. and Jegla, D. *Regulation of extent of vegetative development of the maize shoot meristem* 63
Ito, M., Marie-Claire, C., Sakabe, M., Ohno, T., Hata, S., Kouchi, H., Hashimoto, J., Fukuda, H., Komamine, A. and Watanabe, A. *Cell-cycle-regulated transcription of A- and B-type plant cyclin genes in synchronous cultures* 983
Iwabuchi, M. *see* Ohtsubo, N.

Jack, T., Sieburth, L. and Meyerowitz, E. *Targeted misexpression of AGAMOUS in whorl 2 of* Arabidopsis *flowers* 825
Jacobs, A. *see* De Neve, M.
Jarvis, P., Belzile, F. and Dean, C. *Inefficient and incorrect processing of the Ac transposase transcript in iae1 and wild-type* Arabidopsis thaliana 921
Jarvis, P., Belzile, F., Page, T. and Dean, C. *Increased* Ac *excision (iae): Arabidopsis thaliana mutations affecting* Ac *transposition* 907
Jegla, D. *see* Irish, E.
Jensen, A.B. *see* Busk, P.K.
Jensen, T.J. *see* Borg, S.
Jones, J.D.G. *see* Klimyuk, V.I.
Jones, R.L. *see* Bethke, P.C.
Jordana, X. *see* Stange, C.

Kahn, R.A. *see* Bak, S.
Kalla, R. *see* Tingay, S.
Kamiya, Y. *see* Ait-Ali, T.
Kampfenkel, K. *see* Neuhaus, H.E.
Kandasamy, M.K. *see* Conner, J.A.
Kang, B.G. *see* Kim, J.H.
Kapoor, S., Suzuki, J.Y. and Sugiura, M. *Identification and functional significance of a new class of non-consensus-type plastid promoters* 327
Kaya, H. *see* Ohtsubo, N.
Keller, B. *see* Feuillet, C.
Kendrick, R.E. *see* Weller, J.L.
Kennard, W. *see* Lapitan, N.L.V.
Kerhoas, L. *see* Beveridge, C.A.
Kim, H.-S. *see* Serikawa, K.A.
Kim, J.H., Kim, W.T., Kang, B.G. and Yang, S.F. *Induction of 1-aminocycloprcpane-1-carboxylate oxidase mRNA by ethylene in mung bean hypocotyls: involvement of both protein phosphorylation and dephosphorylation in ethylene signaling* 399
Kim, S.Y., Chung, H.J. and Thomas, T.L. *Isolation of a novel class of bZIP transcription factors that interact with ABA-responsive and embryo-specification elements in the Dc3 promoter using a modified yeast one-hybrid system* 1237
Kim, W.T. *see* Kim, J.H.
Kindle, K.L. *see* Adam, G.
Kindle, K.L. *see* Suzuki, H.
Klessig, D.F. *see* Conrath, U.
Klessig, D.F. *see* Dempsey, D.A.
Klessig, D.F. *see* Takahashi, H.
Klimyuk, V.I. and Jones, J.D.G. AtDMC1, the Arabidopsis *homologue of the yeast* DMC1 *gene: characterization, transposon-induced allelic variation and meiosis-associated expression* 1
Kloti, A. *see* Burkhardt, P.K.
Knight, J.S. *see* Mould, R.M.
Knudson, D.L. *see* Lapitan, N.L.V.
Kobayashi, I. *see* Kobayashi, Y.
Kobayashi, Y., Kobayashi, I., Funaki, Y., Fujimoto, S., Takemoto, T. and Kunoh, H. *Dynamic reorganization of microfilaments and microtubules is necessary for the expression of non-host resistance in barley* 525
Kohler, R.H., Zipfel, W.R., Webb, W.W. and Hanson, M.R. *The green fluorescent protein as a marker to visualize plant mitochondria* in vivo 613
Komamine, A. *see* Ito, M.
Kondorosi, A. *see* Coba de la Pena, T.
Kondorosi, A. *see* Savoure, A.
Kondorosi, E. *see* Savoure, A.
Kononov, M.E., Bassuner, B. and Gelvin, S.B. *Integration of T-DNA binary vector 'backbone' sequences into the tobacco genome: evidence for multiple complex patterns of integration* 945

Kopka, J., Provart, N.J. and Müller-Röber, B. *Potato guard cells respond to drying soil by a complex change in the expression of genes related to carbon metabolism and turgor regulation* 871
Kosslak, R.M., Chamberlin, M.A., Palmer, R.G. and Bowen, B.A. *Programmed cell death in the root cortex of soybean root necrosis mutants* 729
Kouchi, H. *see* Ito, M.
Kunoh, H. *see* Kobayashi, Y.

Lacombe, E., Hawkins, S., Van Doorsselaere, J., Piquemal, P., Goffner, D., Poeydomenge, O., Boudet, A.-M. and Grima-Pettenati, J. *Cinnamoyl CoA reductase, the first committed enzyme of the lignin branch biosynthetic pathway: cloning, expression and phylogenetic relationships* 429
Lamb, C.J. *see* Faktor, O.
Lambert, G.M. *see* Grebenok, R.J.
Lapitan, N.L.V., Brown, S.E., Kennard, W., Stephens, J.L. and Knudson, D.L. *FISH physical mapping with barley BAC clones* 149
Last, R.L. *see* Rose, A.B.
Latham, J.R., Saunders, K., Pinner, M.S. and Stanley, J. *Induction of plant cell division by beet curly top virus gene C4* 1273
Laudie, M. *see* Cooke, R.
Laudie, M. *see* Gallois, P.
Lauerer, M. *see* Scheible, W.-R.
Le, Q.V. *see* Franche, C.
Leah, R. *see* Rouster, J.
Learned, R.M. and Connolly, E.L. *Light modulates the spatial patterns of 3-hydroxy-3-methylglutaryl coenzyme A reductase gene expression in* Arabidopsis thaliana 499
Lemaux, P.G. *see* McElroy, D.
Lenehan, Z. *see* Schmidt, R.
Levy, S., Maclachlan, G. and Staehelin, L.A. *Xyloglucan sidechains modulate binding to cellulose during* in vitro *binding assays as predicted by conformational dynamics simulations* 373
Lindsey, K. *see* Wei, W.
Liu, B., Segal, G., Vega, J.M., Feldman, M. and Abbo, S. *Isolation and characterization of chromosome-specific DNA sequences from a chromosome arm genomic library of common wheat* 959
Liu, Y. *see* Takahashi, H.
Lloyd, J.R. *see* Tomlinson, K.L.
Loake, G. *see* Faktor, O.
Long, D., Goodrich, J., Wilson, K., Sundberg, E., Martin, M., Puangsomlee, P. and Coupland, G. Ds *elements on all five* Arabidopsis *chromosomes and assessment of their utility for transposon tagging* 145
Lopez-Meyer, M. and Nessler, C.L. *Tryptophan decarboxylase is encoded by two autonomously regulated genes in* Camptotheca acuminata *which are differentially expressed during development and stress* 1167
Louwerse, J.D. *see* McElroy, D.
Love, K. *see* Schmidt, R.
Lue, W.-L. *see* Wang, S.-M.

Maathuis, F.J.M., Taylor, A.R., Assmann, S.M. and Sanders, D. *Seal-promoting solutions and pipette perfusion for patch clamping plant cells* 891
Maclachlan, G. *see* Levy, S.
Makaroff, C.A. *see* Peirson, B.N.
Makishima, T. *see* Gallois, P.
Mariani, C. *see* Vriezen, W.H.
Marie-Claire, C. *see* Ito, M.
Martin, C. *see* Chatterjee, M.
Martin, D.J., Firek, S., Moreau, E. and Draper, J. *Alternative processing of the maize* Ac *transcript in* Arabidopsis 933
Martin, M. *see* Long, D.
Martin, T., Hellmann, H., Schmidt, R., Willmitzer, L. and Frommer, W.B. *Identification of mutants in metabolically regulated gene expression* 53
Martin-Canadell, A. *see* Choisne, N.
Martinez-Laborda, A. *see* Serikawa, K.A.
Masgrau, C., Altabella, T., Farras, R., Flores, D., Thompson, A.J., Besford, R.T. and Tiburcio, A.F. *Inducible overexpression of oat arginine decarboxylase in transgenic tobacco plants* 465
Maule, A.J. *see* Wang, D.
McClure, B. *see* Zurek, D.M.
McCouch, S.R. *see* Meijer, A.H.
McElroy, D. *see* Tingay, S.
McElroy, D., Louwerse, J.D., McElroy, S.M. and Lemaux, P.G. *Development of a simple transient assay for* Ac/Ds *activity in cells of intact barley tissue* 157
McElroy, S.M. *see* McElroy, D.
McKhann, H.I. *see* Coba de la Pena, T.
McPherson, J. *see* Orvar, B.L.
Meijer, A.H., Scarpella, E., van Dijk, E.L., Qin, L., Taal, A.J.C., Ruen, S., Harrington, S.E., McCouch, S.R., Schilperoort, R.A. and Hoge, J.H.C. *Transcriptional repression by Oshox1, a novel homeodomain leucine zipper protein from rice* 263
Merkle, T. *see* Haizel, T.
Meshi, T. *see* Ohtsubo, N.
Meyer, C. *see* Crete, P.
Meyerowitz, E. *see* Jack, T.
Miginiac, E. *see* Beveridge, C.A.
Mita, S., Murano, N., Akaike, M. and Nakamura, K. *Mutants of* Arabidopsis thaliana *with pleiotropic effects on the expression of the gene for β-amylase and on the accumulation of anthocyanin that are inducible by sugars* 841
Moehs, C.P., Allen, P.V., Friedman, M. and Belknap, W.R. *Cloning and expression of solanidine UDP-glucose glucosyltransferase from potato* 227
Mohlmann, T. *see* Neuhaus, H.E.
Moreau, E. *see* Martin, D.J.
Morikawa, H. *see* Inada, H.
Mou, B. *see* Zurek, D.M.
Mould, R.M., Knight, J.S., Bogsch, E. and Gray, J.C. *Azide-sensitive thylakoid membrane insertion of chimeric chromosome* f *polypeptides imported by isolated pea chloroplasts* 1051
Mullen, J.A. *see* Adam, G.
Müller-Röber, B. *see* Kopka, J.
Mundy, J. *see* Rouster, J.
Muramoto, Y. *see* Nakamura, T.
Murano, N. *see* Mita, S.
Murfet, I.C. *see* Beveridge, C.A.
Murphy, D.J. *see* Piffanelli, P.
Murphy, D.J. *see* Sarmiento, C.

N'Diaye, A. *see* Terzaghi, W.B.
Naeem, M., Tetlow, I.J. and Emes, M.J. *Starch synthesis in amyloplasts purified from developing potato tubers* 1095
Nagy, F. *see* Haizel, T.
Nakamura, K. *see* Mita, S.
Nakamura, T., Yokota, S., Muramoto, Y., Tsutsui, K., Oguri, Y., Fukui, K. and Takabe, T. *Expression of a betaine aldehyde*

dehydrogenase gene in rice, a glycinebetaine nonaccumulator, and possible localization of its protein in peroxisomes 1115
Nakayama, T. *see* Ohtsubo, N.
Nasrallah, J.B. *see* Conner, J.A.
Nasrallah, M.E. *see* Conner, J.A.
Nessler, C.L. *see* Lopez-Meyer, M.
Neuhaus, H.E., Thom, E., Mohlmann, T., Steup, M. and Kampfenkel, K. *Characterization of a novel eukaryotic ATP/ADP translocator located in the plastid envelope of* Arabidopsis thaliana 73
Nishimoto, T. *see* Gallois, P.
Nishimura, M. *see* Inada, H.

Oakes, M.P. *see* Betzner, A.S.
Oguri, y. *see* Nakamura, T.
Ohno, T. *see* Ito, M.
Ohtsubo, N., Nakayama, T., Kaya, H., Terada, R., Shimamoto, K., Meshi, T. and Iwabuchi, M. *Cooperation of two distinct cis-acting elements is necessary for the S phase-specific activation of the wheat histone H3 promoter* 1219
Olsen, C.E. *see* Bak, S.
Orvar, B.L. and Ellis, B.E. *Transgenic tobacco plants expressing antisense RNA for cytosolic ascorbate peroxidase show increased susceptibility to ozone injury* 1297
Orvar, B.L., McPherson, J. and Ellis, B.E. *Pre-activating wounding response in tobacco prior to high-level ozone exposure prevents necrotic injury* 203
Orzaez, D. and Granell, A. *DNA fragmentation is regulated by ethylene during carpel senescence in* Pisum sativum 137
Osborne, B. *see* Wirtz, U.

Packman, L.C. *see* Webster, C.I.
Page, T. *see* Jarvis, P.
Pages, M. *see* Busk, P.K.
Palmer, R.G. *see* Kosslak, R.M.
Palva, E.T. *see* Vidal, S.
Parcy, F. and Giraudat, J. *Interactions between the* ABI1 *and the ectopically expressed* ABI3 *genes in controlling abscisic acid responses in* Arabidopsis *vegetative tissues* 693
Pathirana, M.S. *see* Dempsey, D.A.
Pay, A. *see* Haizel, T.
Peirson, B.N., Bowling, S.E. and Makaroff, C.A. *A defect in synapsis causes male sterility in a T-DNA-tagged* Arabidopsis thaliana *mutant* 659
Pierson, E. *see* Grebenok, R.J.
Piffanelli, P., Ross, J.H.E. and Murphy, D.J. *Intra- and extracellular lipid composition and associated gene expression patterns during pollen development in* Brassica napus 549
Pinner, M.S. *see* Latham, J.R.
Piquemal, P. *see* Lacombe, E.
Platt, K.A. *see* Wang, T.-W.
Poeydomenge, O. *see* Lacombe, E.
Ponce de Leon, I. *see* Vidal, S.
Potrykus, I. *see* Burkhardt, P.K.
Pottosin, I.I. *see* Tikhonova, L.I.
Poulsen, C. *see* Borg, S.
Provart, N.J. *see* Kopka, J.
Puangsomlee, P. *see* Long, D.
Pwee, K.-H. *see* Webster, C.I.

Qin, L. *see* Meijer, A.H.

Rameau, C. *see* Beveridge, C.A.
Ramirez, I. *see* Stange, C.
Ratet, P. *see* Savoure, A.
Ratnayake, C. *see* Wang, T.-W.
Raynal, M. *see* Cooke, R.
Reid, J.B. *see* Ait-Ali, T.
Reid, J.B. *see* Weller, J.L.
Reijnen, W.H. *see* van Eldik, G.J.
Rhodes, M.J.C. *see* Clark, L.J.
Risseeuw, R., Franke-van Dijk, M.E.I. and Hooykaas, P.J.J. *Gene targeting and instability of* Agrobacterium *T-DNA loci in the plant genome* 717
Rogers, J.C. *see* Rogers, S.W.
Rogers, S.W., Burks, M. and Rogers, J.C. *Monoclonal antibodies to barley aleurain and homologs from other plants* 1359
Roitsch, T. *see* Ehness, R.
Rojo, R. *see* Dammann, C.
Rose, A.B. and Last, R.L. *Introns act post-transcriptionally to increase expression of the* Arabidopsis thaliana *tryptophan pathway gene PAT1* 455
Ross, J.H.E. *see* Piffanelli, P.
Ross, J.H.E. *see* Sarmiento, C.
Rouster, J., Leah, R., Mundy, J. and Cameron-Mills, V. *Identification of a methyl jasmonate-responsive region in the promoter of a lipoxygenase 1 gene expressed in barley grain* 513
Ruen, S. *see* Meijer, A.H.
Ruiter, R.K. *see* van Eldik, G.J.

Saedler, H. *see* Zachgo, S.
Sakabe, M. *see* Ito, M.
Sallaud, C. *see* Savoure, A.
Sanchez-Serrano, J.J. *see* Dammann, C.
Sanders, D. *see* Maathuis, F.J.M.
Sarmiento, C., Ross, J.H.E., Herman, R. and Murphy, D.J. *Expression and subcellular targeting of a soybean oleosin in transgenic rapeseed. Implications for the mechanism of oil-body formation in seeds* 783
Satiat-Jeunemaitre, B. *see* Gomord, V.
Saunders, K. *see* Latham, J.R.
Sauter, M. *Differential expression of a CAK (cdc2-activating kinase)-like protein kinase, cyclins and* cdc2 *genes from rice during the cell cycle and in response to gibberellin* 181
Savoure, A., Sallaud, C., El-Turk, J., Zuanazzi, J., Ratet, P., Schultze, M., Kondorosi, A., Esnault, R. and Kondorosi, E. *Distinct response of* Medicago *suspension cultures and roots to Nod factors and chitin oligomers in the elicitation of defense-related responses* 277
Scarpella, E. *see* Meijer, A.H.
Schachermayr, G. *see* Feuillet, C.
Schaefer, D.G. and Zryd, J.-P. *Efficient gene targeting in the moss* Physcomitrella patens 1195
Scheible, W.-R., Lauerer, M., Schulze, E.-D., Caboche, M. and Stitt, M. *Accumulation of nitrate in the shoot acts as a signal to regulate shoot–root allocation in tobacco* 671
Schilperoort, R.A. *see* Meijer, A.H.
Schlaman, H.R.M. and Hooykaas, P.J.J. *Effectiveness of the bacterial gene* codA *encoding cytosine deaminase as a negative selectable marker in* Agrobacterium*-mediated plant transformation* 1377
Schledz, M. *see* Burkhardt, P.K.
Schmidt, R. *see* Martin, T.
Schmidt, R., Love, K., West, J., Lenehan, Z. and Dean, C. *Description of 31 YAC contigs spanning the majority of* Arabidopsis thaliana *chromosome 5* 563
Schofer, C. *see* Wanzenbock, E.-M.

Schoknecht, G. *see* Tikhonova, L.I.
Schrauwen, J.A.M. *see* van Eldik, G.J.
Schultze, M. *see* Savoure, A.
Schulze, E.-D. *see* Scheible, W.-R.
Schwarz-Sommer, Z. *see* Zachgo, S.
Schweizer, D. *see* Wanzenbock, E.-M.
Segal, G. *see* Liu, B.
Seki, M. *see* Inada, H.
Serikawa, K.A. and Zambryski, P.C. *Domain exchanges between KNAT3 and KNAT1 suggest specificity of the kn1-like homeodomains requires sequences outside of the third helix and N-terminal arm of the homeodomain* 863
Serikawa, K.A., Martinez-Laborda, A., Kim, H.-S. and Zambryski, P.C. *Localization of expression of* KNAT3*, a class* 2 knotted1*-like gene* 853
Sheridan, W.F. and Huang, B.-Q. *Nuclear behavior is defective in the maize (*Zea mays *L.) lethal ovule2 female gametophyte* 1029
Shimamoto, K. *see* Ohtsubo, N.
Sieburth, L. *see* Jack, T.
Silva, H. *see* Conrath, U.
Small, I. *see* Choisne, N.
Smeekens, S. *see* Vijn, I.
Smith, A.M. *see* Tomlinson, K.L.
Smith, F.W., Ealing, P.M., Dong, B. and Delhaize, E. *The cloning of two* Arabidopsis *genes belonging to a phosphate transporter group* 83
Sotta, B. *see* Beveridge, C.A.
Sprenger, M. *see* Feldbrugge, M.
Sprenger, N. *see* Vijn, I.
Staehelin, L.A. *see* Levy, S.
Staehlin, L.A. *The plant ER: a dynamic organelle composed of a large number of discrete functional domains* 1151
Stange, C., Ramirez, I., Gomez, I., Jordana, X. and Holuigue, L. *Phosphorylation of nuclear proteins directs binding to salicylic acid-responsive elements* 1315
Stanley, J. *see* Latham, J.R.
Stein, J.C. *see* Conner, J.A.
Stephens, J.L. *see* Lapitan, N.L.V.
Stern, D.B. *see* Suzuki, H.
Steup, M. *see* Neuhaus, H.E.
Stitt, M. *see* Scheible, W.-R.
Sugiura, M. *see* Kapoor, S.
Sun, C.-W. and Callis, J. *Independent modulation of* Arabidopis thaliana *polyubiquitin mRNAs in different organs and in response to environmental changes* 1017
Sun, T.-P. *see* Ait-Ali, T.
Sundberg, E. *see* Long, D.
Suzuki, H., Ingersoll, J., Stern, D.B. and Kindle, K.L. *Generation and maintenance of tandemly repeated extrachromosomal plasmid DNA in* Chlamydomonas *chloroplasts* 635
Suzuki, J.Y. *see* Kapoor, S.
Swain, S.M. *see* Ait-Ali, T.

Taal, A.J.C. *see* Meijer, A.H.
Takabe, T. *see* Nakamura, T.
Takahashi, H., Chen, Z., Du, H., Liu, Y. and Klessig, D.F. *Development of necrosis and activation of disease resistance in transgenic tobacco plants with severely reduced catalase levels* 993
Takano, M., Egawa, H., Ikeda, J. and Wakasa, K. *The structures of integration sites in transgenic mice* 353
Takemoto, T. *see* Kobayashi, Y.
Tantikanjana, T. *see* Conner, J.A.
Taylor, A.R. *see* Maathuis, F.J.M.
Terada, R. *see* Ohtsubo, N.
Terry, M.J. *see* Weller, J.L.
Terzaghi, W.B., Bertekap, R.L., Cashmore, A.R., N'Diaye, A., Gherbi, H., Gobe, C. and Duhoux, E. *Intracellular localization of GBF proteins and blue light-induced import of GBF2 fusion proteins into the nucleus of cultured* Arabidopsis *and soybean cells* 967
Tetlow, I.J. *see* Naeem, M.
Thom, E. *see* Neuhaus, H.E.
Thomas, T.L. *see* Kim, S.Y.
Thompson, A.J. *see* Masgrau, C.
Thordal-Christensen, H., Zhang, Z., Wei, Y. and Collinge, D.B. *Subcellular localization of H_2O_2 in plants. H_2O_2 accumulation in papillae and hypersensitive response during the barley powdery mildew interaction* 1187
Thornton, S. *see* Tingay, S.
Tiburcio, A.F. *see* Masgrau, C.
Tikhonova, L.I., Pottosin, I.I., Dietz, K.-J. and Schoknecht, G. *Fast-activating cation channel in barley mesophyll vacuoles. Inhibition by calcium* 1059
Ting, J.T.L. *see* Wang, T.-W.
Tingay, S., McElroy, D., Kalla, R., Fieg, S., Wang, M., Thornton, S. and Brettell, R. Agrobacterium tumefaciens*-mediated barley transformation* 1369
Tomlinson, K.L., Lloyd, J.R. and Smith, A.M. *Importance of isoforms of starch-branching enzyme in determining the structure of starch in pea leaves* 31
Tsutsui, K. *see* Nakamura, T.
Twell, D. *see* Wei, W.

van Dijk, E.L. *see* Meijer, A.H.
van Dijken, A. *see* Vijn, I.
Van Doorsselaere, J. *see* Lacombe, E.
van Dun, K. *see* Vijn, I.
van Eldik, G.J., Reijnen, W.H., Ruiter, R.K., van Herpen, M.M.A., Schrauwen, J.A.M. and Wullems, G.J. *Regulation of flavonol biosynthesis during anther and pistil development, and during pollen tube growth in* Solanum tuberosum 105
van Herpen, M.M.A. *see* van Eldik, G.J.
Van Montagu, M. *see* De Neve, M.
van Rijn, C.P.E. *see* Vriezen, W.H.
Vega, J.M. *see* Gotor, C.
Vega, J.M. *see* Liu, B.
Vidal, S., Ponce de Leon, I., Denecke, J. and Palva, E.T. *Salicylic acid and the plant pathogen* Erwinia carotovora *induce defense genes via antagonistic pathways* 115
Vierstra, R.D. *see* Hatfield, P.M.
Vijn, I., van Dijken, A., Sprenger, N., van Dun, K., Weisbeek, P., Wiemken, A. and Smeekens, S. *Fructan of the inulin neoseries is synthesized in transgenic chicory plants (*Cichorium intybus *L.) harbouring onion (*Allium cepa *L.) fructan:fructan 6G-fructosyltransferase* 387
Voesenek, L.A.C.J. *see* Vriezen, W.H.
Voesenek, L.A.C.J. *see* Vriezen, W.H.
von Lintig, J. *see* Burkhardt, P.K.
Vriezen, W.H., van Rijn, C.P.E., Voesenek, L.A.C.J., Voesenek, L.A.C.J. and Mariani, C. *A homolog of the* Arabidopsis thaliana *ERS gene is actively regulated in* Rumex palustris *upon flooding* 1265

Wakasa, K. *see* Takano, M.
Walbot, V. *see* Carle-Urioste, J.C.
Wang, B. *see* Chen, X.
Wang, D. and Maule, A.J. *Contrasting patterns in the spread of two seed-borne viruses in pea embryos* 1333

Wang, M. *see* Tingay, S.
Wang, S.-M., Chu, B., Lue, W.-L., Yu, T.-S., Eimert, K. and Chen, J. adg2-1 *represents a missense mutation in the ADPG pyrophosphorylase large subunit gene of* Arabidopsis thaliana 1121
Wang, T.-W., Balsamo, R.A., Ratnayake, C., Platt, K.A., Ting, J.T.L. and Huang, A.H.C. *Identification, subcellular localization and developmental studies of oleosins in the anther of* Brassica napus 475
Wanzenbock, E.-M., Schofer, C., Schweizer, D. and Bachmair, A. *Ribosomal transcription units integrated via T-DNA transformation associate with the nucleolus and do not require upstream repeat sequences for activity in* Arabidopsis thaliana 1007
Watanabe, A. *see* Ito, M.
Webb, W.W. *see* Kohler, R.H.
Webster, C.I., Packman, L.C., Pwee, K.-H. and Gray, J.C. *High mobility group proteins HMG-1 and HMG-I/Y bind to a positive regulatory region of the pea plastocyanin gene promoter* 703
Wei, W., Twell, D. and Lindsey, K. *A novel nucleic acid helicase gene identified by promoter trapping in* Arabidopsis 1307
Wei, Y. *see* Thordal-Christensen, H.
Weisbeek, P. *see* Vijn, I.
Weisshaar, B. *see* Feldbrugge, M.
Weller, J.L., Terry, M.J., Reid, J.B. and Kendrick, R.E. *The phytochrome-deficient* pcd2 *mutant of pea is unable to convert biliverdin to IXa to 3(Z)-phytochromobilin* 1177
West, J. *see* Schmidt, R.
Whelan, J. *see* Aubert, S.
Wiemken, A. *see* Vijn, I.
Willmitzer, L. *see* Martin, T.
Wilson, K. *see* Long, D.
Wirtz, U., Osborne, B. and Baker, B. Ds *excision from extrachromosomal geminivirus vector DNA is coupled to vector DNA replication in maize* 125
Wobbe, K.K. *see* Dempsey, D.A.
Wu, R. *see* Chen, X.
Wu, S.-C. *see* Ham, K.-S.
Wullems, G.J. *see* van Eldik, G.J.
Wunn, J. *see* Burkhardt, P.K.

Yang, S.F. *see* Kim, J.H.
Yokota, S. *see* Nakamura, T.
Yu, T.-S. *see* Wang, S.-M.

Zachgo, S., Saedler, H. and Schwarz-Sommer, Z. *Pollen-specific expression of DEFH125, a MADS-box transcription factor in* Antirrhinum *with unusual features* 1043
Zambryski, P.C. *see* Serikawa, K.A.
Zambryski, P.C. *see* Serikawa, K.A.
Zhang, Z. *see* Thordal-Christensen, H.
Zipfel, W.R. *see* Kohler, R.H.
Zryd, J.-P. *see* Schaefer, D.G.
Zuanazzi, J. *see* Savoure, A.
Zurek, D.M., Mou, B., Beecher, B. and McClure, B. *Exchanging sequence domains between S-RNases from* Nicotiana alata *disrupts pollen recognition* 797

Subject index

abscisic acid 693, 773, 1237, 1285
Ac 907, 921
Ac transposase 933
ACC oxidase 399
ACC synthase 399
Acer pseudoplatanus 649
Activator 125, 145, 907
acyl lipids 549
adg2 1121
ADPG pyrophosphorylase 1121
Aequorea victoria 573
AGAMOUS 825
Agrobacterium 15, 1369
Agrobacterium tumefaciens 717, 897, 945
aleurain 1359
aleurone cells 363
alleles 1
Allocasuarina verticillata 897
allocation 671
alternative oxidase 649
alternative polyadenylation 933
alternative splicing 933
amber suppressor tRNA *Leu* gene 597
amylopectin 31
amyloplasts 1095
analysis 1387
anther 105
anthocyanin 289, 421, 841
antifungal proteins 169
antisense 993, 1297
apical dominance 339
apoptosis 729
apoptosis suppressor 1325
Arabidopsis thaliana 1, 73, 83, 145, 213, 289, 301, 347, 455, 563, 587, 625, 693, 825, 841, 853, 863, 907, 921, 933, 1007, 1017, 1121, 1127, 1307, 1325
  flowers 53
arginine decarboxylase overexpression 465
as-1 element 1315
ascorbate 1297
ASF-1 factor 1315

β-amylase 841
β-D-glucuronidase (GUS) 1105
β-glucuronidase 53, 597, 897
bacterial artificial chromosome (BAC) 149
barley 149, 157, 525, 1359, 1369
  aleurone 1227
  grain 513
beet curly top virus 1273
betaine aldehyde dehydrogenase 1115
binary vectors 945
blue light photoreceptor 421
branched-chain amino acids 649
Brassica 809
Brassica napus 783
bZIP 967

Ca^{2+}-ATPase gene 363
calcium dependence 1059
calmodulin-like domain protein kinase (CDPK) 1227
Camptotheca acuminata 1167
camptothecin 1167
carbohydrate partitioning 539
carbon metabolism 407
carbonic anhydrase 407
carotenoids 1071
carpel 137
catalase 993
Catharanthus roseus 983
cation channel 1059
catmint 1387
cdc2 181
cdc2-activating kinase (CAK) 181
cDNA 227
cell ablation 587
cell culture 967
cell cycle 181, 983, 1219, 1273
cellular differentiation 237
cellulose 373
cereal rust 45
cereals 1369
chalcone synthase 1079, 1105
chemotypes 1387
chicory 387
chimaeric clone 563
chitinase 169
Chlamydomonas 1341
chlorophyll 1177
chloroplast 1051
chloroplast transformation 635
chromophore 1177
chromosome-specific sequences 959
cinnamoyl CoA reductase 429
cis-elements 53
cloning 443
co-transformation 15
complex of metabolic enzymes 251
confocal microscopy 613
copy correction 635
cotransfection assay 1079
cryptochrome 421
cultured BY-2 tobacco cells 882
cyclin 181, 983
CYP51 191
cysteine biosynthesis 251
cytochrome *f* 1051
cytochrome P450 191
cytokinins 407
cytoplasmic localization 967
cytosine deaminase 717
cytoskeleton 659
cytosolic Ca^{2+} 363

daffodil 1071
DAG 759
Dc3 1237
DEAD/H protein family 1307
defense genes 115
defense response 729
development 1029
developmental regulation 263
diaminobenzidine (DAB) 1187
dihydroflavonol reductase 429
disease lesion mimic mutation 729
Dissociation 125, 145

DNA fragmentation 137
DNA integration 353
DNA markers 563
DNA replication 125
DNA-binding protein 263, 1079, 1207
DOP-PCR 959
dot-blot 1141
drought stress 871
DT-A 1377

E1 213
elicitor 277
elicitor-releasing activity 169
elongated hypocotyl 421
embryo 1237
embryogenesis 289
endoplasmic reticulum 783, 1151
  membrane domains 1151
  retention 313
endosperm-specific promoter 1071
enhancement 455
ent-kaurene synthase A 443
Erwinia carotovora 115
Escherichia coli 73
  expression 191
ethylene 137, 399, 1207, 1265
ethylene response sensor (ERS) 1265
Eucalyptus 429
evolution 959
excision 125
expressed sequence tag 1127
expression 1

female 1029
fertilization 1043
flavonoid 289
flavonol synthase 105
flavonols 105
flooding 1265
floral determination 63
flower development 1043
fluorescence *in situ* hybridization (FISH) 149
fluorescent labelling 1141
fructan 387
fructosyltransferase 387
fruit ripening 1207
functional heterologous expression 73
functional protein domains 251

G-box 1105
gametophyte 1029
GBF 967
GC-rich introns 1253
geminivirus 1273
gene activation 1079
gene amplification 635
gene cloning 1341
gene expression 347, 455, 549, 871, 1307
gene family 213
gene regulation 1027
gene targeting 1195, 1377
gene transfer 1369
gibberellin biosynthesis 443
gibberellin-dependent signalling pathway 363
gibberellins 137
glucanase inhibitor proteins 169
glucocorticoid receptor 605
Glycine max 783
glycinebetaine 1115
glycoalkaloid 227
green fluorescent protein 573, 613
GTP-bound 93
guard cell 693, 871
GUS fusion 455
GUS gene 883

H-box 1105
hcf106 63
herbicides 649
Hex motif 1219
HMG CoA reductase 499
HMG-1 703
HMG-I/Y 703
homeobox 853, 863
homeodomain 853, 863
homeodomain protein 263
homoeologous chromosomes 959
homologous recombination 15, 717, 1195, 1349
hordein genes 149
Hordeum vulgare 149, 1059, 1369
hydrogen peroxide 1187
hyperplasia 1273
hypersensitive response 1187

iae 907
iae1 921
illegitimate recombination 353
immunolocalization 1043
integration 15
interaction 93
intron 455
ion transport 83
iridoid 1387
isoflavonoid 277
isoforms 31

jasmonate 203, 1167
jasmonic acid 773

kanamycin resistance 897
kn1 853, 863
KNAT 853, 863

large subunit 1121
lateral root 729
LbPCR 587
lea gene 1237
leaf rust 45
leaf starch 31
leaves 63
lethal 1029
leucine zipper 1237
light 499
light regulation 967
lignins 429
lipoxygenase 1 gene 513

MADS-box family 1043

maize 1029, 1253, 1285
Ac 157
Ds 157
male gametophyte 549
male sterility 489, 587
male-sterile mutant 659
map-based cloning 563
meiosis 659
membrane integration 1051
membrane protein 83
membrane seal 891
meristem culture 63
methyl jasmonate-responsive region 513
mevalonate 499
microdissection 959
microfilaments 525
microspores 475
microsporocyte 659
microtubules 525, 659
missense mutation 1121
molecular markers 959
monoclonal antibodies 1359
moss 1195
mRNA 399
multigene families 1127
mutant 339, 443, 693, 1121
mutation 1029
MYB recognition element 1079

necrosis 729, 1297
negative selection 717
neokestose 387
nepetalactone 1387
Nicotiana 625, 797
Nicotiana tabacum 327, 597, 1377
nitrate 625, 671
nitrate reductase 625, 671
nitrogen fixation 237
nitrogen starvation 1341
nodulation 277
nodule development 407
nodulins 407
nonhost resistance 525
nuclear targeting 573
nucleic acid helicase 1307

O-acetylserine(thiol)lyase 347
obtusifoliol 191
Oct motif 1219
oil bodies 475, 783
okadaic 773
oleosins 475, 783
one-hybrid system 1237
onion 387
orthologous gene 191
oxidative stress 993
oxygen barrier 407
ozone 203, 1297

papilla 1187
particle bombardment 1349
particle gun 883
patatin 53
patch clamp 891, 1059
pathogenesis-related (PR) proteins 747, 993
pea 443
embryo 1333
shoot 703
peroxidase 1187, 1297
peroxisomes 1115
phase change 63
Phaseolus vulgaris 1105
phosphate transport 83
phosphorylation 1227
photomorphogenesis 421, 1177
photoreceptor 1177
phylogeny 429
Physcomitrella patens 1195
physical mapping 149, 563
phytoalexin 169
phytochrome 421
phytohormones 539
Phytophtora sojae f.sp. glycines 169
pipette perfusion 891
pistil 105
Pisum 443
Pisum sativum 1177
Pisum sativum L. 31, 339
plant cell 313
plant defense 277
plant–microbe interaction 525
plant signal transduction 747
plant transformation 945, 1195, 1349
plastid gene expression 883
plastid promoters 327
plastid RNA polymerase gene (*rpoB*) 883
plastidic ATP/ADP translocator 73
plastocyanin gene promoter 703
plastoglobuli 475
pollen 475
pollen tube growth 105
pollination 797
polyadenylation 921
polyamines 465
polyubiquitin 1017
post-transcriptional regulation 625
potato 227, 773, 1095
powdery mildew 525
programmed cell death 1325
promoter 53, 983
promoter analysis 1285
promoter deletion analysis 883
promoter tagging 1341
promoter trapping 1307
promoter-GUS 853
protein cross-linking 1187
protein dephosphorylation 399
protein kinase inhibitors 747
protein phosphatase inhibitors 747
protein phosphorylation 399, 1315
protein phosphorylation/dephosphorylation 747
protein targeting 1051
proteinase inhibitor II 773
proteolysis 213
protoplast transformation 1377
putrescine 465

quality control 313

rab17 1285
radial spoke protein 1341
Ran 93
RanBP 93
Ras superfamily 237
rearrangement 353
RecA-like gene 1
receptor 1265
receptor-like kinase 45
reduced transposition frequency 933
regulation 499, 671
repeated sequence elements 1007
resistance 301
resistance gene 45
reticuloplasmin 313
retrofitting 1349
Rhizobium 277
ribosomal DNA transcription 1007
ribosomal intergenic region 1007
ribosomal protein 1127
ribosome tagging 1007
rice 263, 1115
rice (*Oryza sativa*) 181
RNA splicing 443
root cortex 729
root–shoot communication 339
Rumex palustris 1265

25S rRNA 1007
S phase-specific expression 1219
S-locus genes 809
S-RNase 797
SA
salicylic acid 115, 203, 747, 993, 1315
SecA 1051
seed coat 289
seed development 443
seed-borne viruses 1333
self-incompatibility 717, 797, 809
senescence 137
sensitivity 693
serine–threonine kinase 45
shoot:root 671
signal transduction 53, 237
signalling 203
sink–source regulation 539
Solanum tuberosum 105, 871
somaclonal variation 717
specificity 863
spectinomycin 327
splicing efficiency 1253
sporamin 313
starch synthesis 31, 1095
starch-branching enzyme 31
sterol 14α-demethylase 191
stilbene synthase genes 489
stop codon suppression 587
streptomycin 327
stress 1017, 1265
subcellular localization 1187
substrates 1095
sugar-inducible expression 841
sulfur metabolism 251, 347
sulphorhodamine 1141
suppressible allele 759
SV ion channel 1227
symbiosis 277
symptom determinant 1273
synchronization 181
synchronous culture 983

T-DNA 15
  borders 945
  integration 717, 945
  DNA tagging 1307
tagetitoxin 327
tagging 907
Tam3 759
tapetum 475, 549
targeting 783
tassel 63
tetracycline-inducible promoter 465
tetrapyrrole 1177
thylakoid 1051
tissue specificity 1273
tissue-specific elements 1105
tobacco 202, 465, 489, 983, 1297, 1315, 1377
tomato 1207
toxic gene 1377
transactivation 1207
transactivation system 597
transcription factor 263, 967
transcriptional activation 1315
transcriptional regulation 327
transcriptional repression 263
transformation 157, 897, 1369
transgene structure 353
transgene-induced silencing 809
transgenic plant
transgenic plants 15, 387, 465, 605, 625, 693
transgenic rice 353, 1071
transglycosylation 1141
transparent testa 289
transposable elements 1, 759
transposition 125, 157
transposon 907, 921
transposon tagging 145
trichome 347, 1387
tRNA 587
tryphine 549
tryptophan 455
tryptophan decarboxylase 1167
tuber wounding 227
tubers 1095
turnip crinkle virus (TCV) 301
two-hybrid system 93, 251
type I element 1219

ubiquitin 213, 1017
ubiquitin-activating enzyme 213

vacuolar membrane 1059
vacuolar targeting 313
vesicle transport 237
vitamin A deficiency 1071
voltage dependence 1059

wheat 45, 959

wheat dwarf virus 125
  replicon 157
wheat histone H3 gene 1219
whorl 2 825
wounding 203, 773

xylem sap 339
xyloglucan 373, 1141
xyloglucan endotransglycosylase (XET) 1141

yeast 73, 227
yeast artificial chromosome (YAC) 563, 1349